



SEQUENCE LISTING

<110> BESEME, Frederic

BLOND, Jean-Luc

BOUTON, Olivier

MANDRAND, Bernard

MALLET, Francois

PERRON, Herve

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<141> 1999-12-16

<150> PCT/FR98/01442

<151> 1998-07-06

<150> FR 97/08815

<151> 1997-07-07

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<170> PatentIn version 3.0

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<211> 2585

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<213> Human

<220>

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<222> (833)..(833)

<223> n = any nucleotide

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<211> 2575

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<213> Human

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<211> 783

<212> DNA

<213> Human

<220>

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<223> n = any nucleotide

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<222> (563)..(563)

<223> n = any nucleotide

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<211> 21

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<210> 19

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<220>

<223> PCR primers or probe

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<212> DNA

<213> Artificial

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<223> PCR primers or probe

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<210> 21

<211> 22

<212> DNA

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<223> PCR primers or probe

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<210> 22

<211> 20

<212> DNA

<213> Artificial

<220>

<223> PCR primers or probe

<400> 22

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<210> 23

<211> 20

<212> DNA

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<211> 22

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<210> 26

<211> 22

<212> DNA

<213> Artificial

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<223> Probe or primer

<400> 26

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<211> 24

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<223> Probe or primer

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<211> 21

<212> DNA

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<223> Probe or primer

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21

<210> 29

<211> 678

<212> DNA

<213> Artificial

<220>

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<220>

<221> misc_feature

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180

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<211> 536

<212> DNA

<213> Artificial

<220>

<223> Pgag-LB19 probe

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ggctatattg atgttttaca aggattagga caatcctttg atctgacatg gagagatata	300
atattactgc taaatcagac gctaacctca aatgagagaa gtgctgccat aactggagcc	360
cgagagtttg gcaatctctg gtatctcagt caggtcaatg ataggatgac aacggaggaa	420
agagaacgat tccccacagg gcagcaggca gttcccagtg tagctcctca ttgggacaca	480
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<212> DNA

<213> Artificial

<220>

<223> Penv-C15 probe

<400> 31

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gcattggcag tatcacaacc tctactcagt tctactacaa actatctcaa gaaataaatg	180
gtgacatgga acaggtcact gactccctgg tcaccttgca agatcaactt aactccctag	240
cagcagtagt ccttcaaaat cgaagagctt tagacttgct aaccgcaaaa agagggggaa	300
cctgtttatt tttaggagaa gaacgctggt attatgttaa tcaatccaga attgtcactg	360
agaaagttaa agaaattcga gatcgaatac aatgtagagc agaggagctt caaaacaccg	420
aacgctgggg cctcctcagc caatggatgc cctgggttct ccccttctta ggacctctag	480
cagctctaatt attgttactc ctctttggac cctgtatctt taacctcctt gttaagtttg	540
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<210> 32

<211> 364

<212> DNA

<213> Artificial

<220>

<223> Ppro-E probe

<400> 32

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gacactggcg cagccttctc agtcttactt tctgtccca gacaattgtc ctccagatct 180

gtcactatcc gaggggtcct aggacagcca gtcactacat acttctctca gccactaagt 240

tgtgactggg gaactttact cttttcacat gcttttctaa ttatgcctga aagccccact 300

cccttgttag ggagagacat tttagcaaaa gcaggggccca ttatacacct gaacaagctt 360

gaaa 364

<210> 33

<211> 538

<212> PRT

<213> Human

<400> 33

Met Gly Leu Pro Tyr His Ile Phe Leu Cys Ser Val Leu Ser Pro Cys

1

5

10

15

Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
20 25 30

Pro His Pro Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
35 40 45

Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
115 120 125

Val Lys Glu Val Ile Ser Gln Leu Thr Gly Val His Gly Thr Ser Ser
130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
210 215 220

Ser Asn Val Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
290 295 300

Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln

340

345

350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu

355

360

365

Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Arg Asn Arg Arg

370

375

380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu

385

390

395

400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu

405

410

415

Lys Val Glu Glu Ile Pro Asp Arg Ile Gln Arg Ile Ala Glu Glu Leu

420

425

430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Arg Trp Met Pro Trp Ile

435

440

445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe

450

455

460

Gly Pro Cys Ile Phe Asp Leu Leu Val Asn Phe Val Ser Ser Arg Ile

465

470

475

480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys

485

490

495

Ile Tyr Arg Arg Pro Leu Asp Arg Pro Ala Ser Pro Arg Ser Asp Val

500

505

510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro

515

520

525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser

530

535

<210> 34

<211> 52

<212> PRT

<213> Human

<400> 34

Met Glu Pro Lys Met Gln Ser Lys Thr Lys Ile Tyr Arg Arg Pro Leu

1

5

10

15

Asp Arg Pro Ala Ser Pro Arg Ser Asp Val Asn Asp Ile Lys Gly Thr

20

25

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Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro Leu Leu Arg Pro Asn Ser

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40

45

Ala Gly Ser Ser

50

<210> 35

<211> 48

<212> PRT

<213> Human

<400> 35

Met Leu Met Thr Ser Lys Ala Pro Leu Leu Arg Lys Ser Gln Leu His
1 5 10 15

Asn Leu Tyr Tyr Ala Pro Ile Gln Gln Glu Ala Val Arg Ala Val Val
20 25 30

Gly Gln Pro Pro Gln Gln His Leu Gly Phe Pro Val Glu Met Gly Asp
35 40 45

<210> 36

<211> 20

<212> DNA

<213> Unknown

<220>

<223> Splice donor site

<400> 36

atccaaagtg gtgagtaata

20

<210> 37

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<212> DNA

<213> Unknown

<220>

*B3
conc'd*
<223> Splice acceptor site

<400> 37

cttttttcag atgggaaacg

20